REMARKS

Claims 1-43 are pending in the present application.

The rejections of: (a) Claims 1-3 under 35 U.S.C. §102(b) over Town et al, (b) Claims 1-5, 9-11, 19-21, 25-27, and 42 under 35 U.S.C. §102(b) over Dormann et al, and (c) Claims 1-11, 19-27, and 42 under 35 U.S.C. §102(e) over La Rosa et al, are obviated by amendment.

Applicants submit that none of Town et al, Dormann et al, or La Rosa et al disclose or suggest a polynucleotide falling within the scope of the claimed invention. Specifically, the sequences disclosed by Town et al have 63.7% homology on a nucleotide sequence level and 71.4% homology on an amino acid level. The sequences disclosed by Dormann et al have 63.2% homology on a nucleotide sequence level and 71.1% homology on an amino acid level. Further, the sequence disclosed by La Rosa et al has 90.1% homology on an amino acid level. Evidence for the same is provided by the Sequence Alignments **submitted herewith**. In view of the foregoing, the claimed invention is not anticipated by the cited references.

Withdrawal of these grounds of rejection is requested.

The rejections of: (a) Claims 1-11, 19-27, and 42 under 35 U.S.C. §112, first paragraph (enablement), and (b) Claims 1-11, 19-27, and 42 under 35 U.S.C. §112, first paragraph (written description), are believed to be obviated by amendment.

Indeed, it is the current trend in U.S. patent examination to narrow the permissible scope of homologs when DNA or protein sequences are claimed. This case falls right in line with this trend. Nonetheless, Applicants wish to direct the Examiner's attention to a recent decision by the U.S. PTO's Board of Patent Appeals and Interferences (*Ex parte Bandman*,

enclosed herewith) in which the Board held that claims to amino acid sequences that are at least 95% homologous to the disclosed sequence are adequately described and enabled when the specification describes the nucleotide and amino acid sequences.

As in *Ex parte Bandman*, the present specification provides the amino acid sequence (SEQ ID NO: 2) and the polynucleotide encoding the same (i.e., SEQ ID NO: 1). Moreover, the claims specify the activity required for all proteins encoded by the claimed polynucleotide that fall within the scope thereof. Clearly if the Board finds that under similar circumstances to the present specification an amino acid sequence having at least 95% homology is adequately described and enabled, the certainly so too is the homology of the present application.

Further, with respect to the sufficiency of the disclosure for describing the claimed sequence, the Examiner's attention is directed to Example 14 of the Synopsis of Application of Written Description Guidelines which analyzes a situation where a claim covers a protein that is at least 95% identical to a disclosed sequence and has a specific function. In these guidelines, the Patent Office has concluded that such a claim is adequately described within the meaning of 35 U.S.C. § 112, first paragraph

> There is actual reduction to practice of the single disclosed species. The specification indicates that the genus of proteins that must be variants of SEQ ID NO: 3 does not have substantial variation since all of the variants must possess the specified catalytic activity and must have at least *95%* identity to the reference sequence, SEQ ID NO: 3. The single species disclosed is representative of the genus because all members have at least *95%* structural identity with the reference compound and because of the presence of an assay which applicant provided for identifying all of the at least *95%* identical variants of SEQ ID NO: 3 which are capable of the specified catalytic activity. One of skill in the art would conclude that applicant was in possession of the necessary common attributes possessed by the members of the genus.

Conclusion: The disclosure meets the requirements of 35 USC §112 first paragraph as providing adequate written description for the claimed invention.

As the specification adequately describes the sequences that at least 95% homologous to SEQ ID NO: 2, a polynucleotide that is at least 95% homologous to SEQ ID NO: 1, and the specification describes how one can test for the recited activity to readily determine whether the variants are capable of the specified catalytic activity. Therefore, the claims as presented herein are deemed to be fully described and enabled.

Withdrawal of these grounds of rejection is requested.

The rejection of Claims 1-11, 19-27, and 42 under 35 U.S.C. §112, second paragraph, is obviated by amendment.

With respect to "stringent conditions" this language has been deleted in favor of the homology values recited in page 13, lines 19-28 used to define the "stringent conditions". The term "gene" has been replaced with "polynucleotide". Claims 11, 27, and 42 have been amended to ensure that all essential steps are recited.

Applicants request withdrawal of this ground of rejection.

The rejection of Claims 1-2, 11, and 27 under 35 U.S.C. §101 is obviated by amendment.

Claims 1 and 2 have been amended to define the polynucleotide as being "isolated".

Withdrawal of this ground of rejection is requested.

The objection to the specification is obviated by the amendment to the description of Figure 4 and the submission of the enclosed substitute Sequence Listing. Applicants **submit**

herewith a substitute Sequence Listing and a corresponding computer-readable Sequence Listing. The sequence information recorded in the corresponding computer-readable Sequence Listing is identical to the paper copy of the substitute Sequence Listing. Support for all of the sequences listed in the substitute Sequence Listing is found in the present application. No new matter is believed to have been introduced by the submission of the substitute Sequence Listing and the corresponding computer-readable Sequence Listing. The specification has also been amended to add sequence identifiers where necessary. Support for this amendment is provided by the originally filed specification and Sequence Listing.

Finally, the objection to the drawings is obviated in part by amendment and traversed in part.

To address the criticism in paragraphs 5 and 6 of the Office Action, Applicants have amended the description of Figures 6-8, 10, 11, 13, and 16. Therefore, this objection is believed to be moot.

In paragraph 7 of the Office Action, the Examiner alleges that Figure 17 fails to comply with 37 CFR 1.84(g) "because it is framed". Applicants disagree with this allegation by the Examiner. Fig. 17 shows the results of genomic Southern hybridization described in Example 8. The solid line in Figure 17 is not a "frame" as the Examiner alleges, but rather is an illustration of the outer boundary of the membrane to which the content of the electrophoretic gel was transferred. Thus, the solid line in Figure 17 is not a "frame", but rather a part of the illustration. In view of the foregoing, Applicants submit that Figure 17 is in compliance with 37 CFR 1.84(g) and that this ground of rejection should be withdrawn.

Also, in paragraph 7, the Examiner alleges that the molecular size markers are missing for Figure 17. At the outset, it should be noted that there is no requirement in U.S.

patent practice for an electrophoretic gel to contain molecular size markers. This is especially true where the description in the specification clearly explains the detail of what is illustrated in the Figure. In this case, the description in Example 8 (see pages 44-45) sufficiently describes Figure 17 and what is shown therein. Further, the Examiner should be mindful of the fact that Figure 17 shows the results of a Southern hybridization assay where the probe is the kanamycin-tolerant (NPT) gene region of pBI121 labeled with Alphos Direct. Thus, following hybridization and detection, any molecular size markers present in the original electrophoretic gel would not be detected. In view of the foregoing, Applicants submit that Figure 17 is proper and complete.

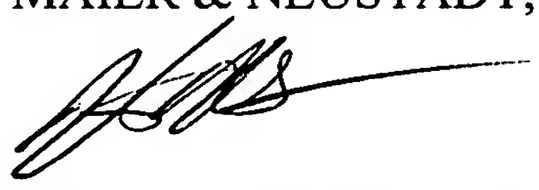
In paragraph 8, the Examiner alleges that the molecular size markers are missing for Figure 18. This allegation is incorrect as it is noted that the molecular size markers are flanking lanes 1 and 6. Thus, this objection is without merit.

Applicants request withdrawal of these grounds of objection.

Applicants submit that the present application is in condition for allowance. Early notification to this effect is respectfully requested.

Respectfully submitted,

OBLON, SPIVAK, McCLELLAND,
MAIER & NEUSTADT, P.C.



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(OSMMN 08/03)

```
[ GENETYX-MAC : Nucleotide Sequence Homology Data ]

Date : 2007.07.27

1st Nucleotide Sequence
  File Name          : PsUGE1
  Sequence Size      : 1094

2nd Nucleotide Sequence
  File Name          : Doremann and Bennig DNA
  Sequence Size      : 1356

  Unit Size to Compare = 4
  Pick up Location     = 5


[63.2% / 1023 bp]     INT/OPT.Score : <   1604/  1836 >

     1'                                                    ATG

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     4' GCGATCGGCGGGGCGGAGGCCGGCGGGGGAGGCGCGGGGGCCAGCGGCCGGAGCGTGCTG
                                                      * ** * * **
   121" TCTTCTTGATAACCTTTCTTCTTCTTTGAAATGGGTTCTTCTGTGGAGCAGAACATTCTT

    64' GTGACGGGCGGCGCGGGGTTCATCGGCACGCACACGGCGCTGCGCCTGCTGGAGCAGGGC
        ** ** ** ** ** ** ** ***** ***** ** *   * *  ** **  *  * **
   181" GTTACTGGTGGTGCTGGCTTTATCGGGACGCATACTGTTGTTCAACTTCTCAAAGATGGT

   124' TACGGCGTCACCGTCGTCGACAACTTCCACAACTCCGTCCCCGAGGCGCTCGAACGCGTC
        *     **  *  ** **** ** **  * ***** **  * ** ** * **  * **
   241" TTTAAGGTTTCGATCATCGATAATTTTGATAACTCTGTTATCGAAGCTGTTGATAGAGTT

   184' CGCCTCATCGCCGGGCCCGCGCTCTCCGCCCGCCTCGACTTCATCCGGGGGGATCTGAGG
        *     * *  ** ** *  ******      **********  * *** ***** **
   301" AGGGAGCTTGTTGGTCCTGATCTCTCCAAGAAGCTCGACTTCAATCTGGGTGATCTAAGA

   244' AGCGCCGGGGACTTGGAGAAGGCGTTCGCGGCCAGGAGGTACGACGCCGTCGTCCACTTC
        * *   ****** * *****    *** *      *** *  ** ** **  * ** **
   361" AACAAAGGGGACATTGAGAAACTATTCTCCAAGCAGAGATTTGATGCTGTGATTCATTTT

   304' GCGGGGCTCAAGGCCGTCGGGGAGAGCGTCGCGCGCCCGGACATGTACTACGAGAACAAC
        ***** ** ** ** ** ** ***** ** *          *   ****  ** ** ***
   421" GCGGGTCTTAAAGCTGTGGGTGAGAGTGTTGAAAAGGGTCGCCGCTACTTTGACAATAAC

   364' CTCGCCGGCACCATCAACCTCTACAAGGCCATGAACGAGCACGGCTGCAAGAAGATGGTG
        * *  ** ** ***** ** **  ** *****    ** **  ****** * *******
   481" TTGGTTGGAACAATCAATCTATATGAGACCATGGCAAAGTACAACTGCAAAATGATGGTG

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        ** ** ** ** ** ** ** ** **    ** **   *** ** *** * ** ****
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   484' AAGCTGCAGGCCGCCAACCCCTACGGCAGGACCAAGCTCATCCTGGAGGAGTTGGCGCGG
        * * ****   ** ** ** **  * ** ****** * ** ** **  * **  *
   601" GAATTAAAGGCTATGAATCCTTATGGTCGTACTAAGCTCTTTCTTGAAGAAATAGCTAGA

   544' GACTACCAGCGCGCGGACCCGGGCTGGAGCATCGTCCTGCTGCGCTACTTCAACCCCATC
        **    **    ** ** **** ***** **  * ****** * ******** **  *
   661" GATATTCAAAAGGCAGAACCGGAATGGAGAATTATTCTGCTGAGGTACTTCAATCCTGTA

   604' GGCGCCCACAGCTCCGGCGAGATCGGCGAGGACCCCAAGGGGGTGCCCAACAACCTGCTG
        ** ** **       ***   ** ** ***** ** ** **  * ***** *****  **
   721" GGAGCACATGAGAGTGGCAGTATTGGTGAGGATCCAAAAGGCATCCCCAATAACCTCATG

   664' CCCTACATCCAGCAGGTCGCCGTCGGCAGGCTCCCCGAGCTCAACGTCTACGGCCACGAT
        ** ******** ** ** ***** **  *  * ** ** ***** ***** ** ** **
   781" CCTTACATCCAACAAGTGGCCGTTGGACGTTTACCGGAACTCAATGTCTATGGACATGAC
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  724' TACCCCACCCGTGACGGCACCGCGATCAGGGACTACATACACGTCGTCGACCTGGCCGAC
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  841" TATCCCACCGAGGATGGTAGTGCGGTAAGAGACTACATCCATGTGATGGATTTAGCAGAT

  784' GGGCACATCGCGGCGCTGAACAAGCTGTTCGACACTCCTGATTTCGGTTGTGTGGCCTAC
       ** ** ***** ***** *  ***** ** *    ***  *  * ******   ** ***
  901" GGCCATATCGCTGCGCTCAGGAAGCTATTTGCTGATCCAAAGATTGGTTGTACTGCTTAC

  844' AATCTGGGCACAGGGCGCGGCACATCCGTTCTCGAGATGGTGGCGGCGTTCAAGAAGGCA
       ***** ** ** ** *  ** ** ** **  * ** ***** ** ** **  * ** **
  961" AATCTAGGGACTGGTCAAGGAACGTCTGTGTTAGAAATGGTTGCAGCTTTTGAAAAAGCT

  904' TCCGGCAAGGAGATCCCCACCAAGATGTGCCCCAGGAGACCGGGTGACGCGACGGAGGTT
       ********* * ***** *  ***.* ** ** ** **  * ** ** ** ** *  ***
 1021" TCCGGCAAGAAAATCCCGATTAAGCTCTGTCCGAGAAGGTCAGGAGATGCAACAGCAGTT

  964' TACGCGTCCACTGAGAAGGCCGAAAGGGAGCTCGGATGGAGGGCCCAGTATGGAATCGAG
       ** ** ** ** ******** ** *  ** ** ** **** ***  * ****** * **.
 1081" TATGCTTCAACAGAGAAGGCTGAGAAAGAACTTGGCTGGAAGGCAAAATATGGAGTGGAT

 1024' GAGATGTGCAGGGACCAGTGGAACTGGGCCAAGAAGAACCCCTATGGCTACTGCGGCACT
       ********** ** ******** *****    ** ** ** *  ** ***
 1141" GAGATGTGCAGAGATCAGTGGAAATGGGCTTTCAATAATCCATGGGGTTACCAGAATAAG

  1084' GCCGAAAAATA

  1201" CTTTGAATTTACTTCTTTTGTTTGGAGTTACCATTTCTAATTACTCAAATCTAAAAGAAA
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1st Nucleotide Sequence
  File Name         : PsUGE1
  Sequence Size     : 1094

2nd Nucleotide Sequence
  File Name         : Town et al UGE DNA
  Sequence Size     : 1462

  Unit Size to Compare = 4
  Pick up Location     = 5

[63.7% / 1023 bp]     INT/OPT.Score : <   1622/  1866 >

     1'                                                    ATGGC

   121" TGTTCTTCTGTTGGTGGTGGTGATCTAGTTTTCAAAGAATCGATTTTGCCAAGTGGGTTC

    6' GATCGGCGGGGCGGAGGCCGGCGGGGGAGGCGCGGGGGCCAGCGGCCGGAGCGTGCTGGT
                                                       * ** * * ** **
  181" TTCTTGATAACCTTTCTTCTTCTTTGAAATGGGTTCTTCTGTGGAGCAGAACATTCTTGT

   66' GACGGGCGGCGCGGGGTTCATCGGCACGCACACGGCGCTGCGCCTGCTGGAGCAGGGCTA
        ** ** ** ** ** ** ***** ***** ** *   * *  ** **  * * ** *
  241" TACTGGTGGTGCTGGCTTTATCGGGACGCATACTGTTGTTCAACTTCTCAAAGATGGTTT

  126' CGGCGTCACCGTCGTCGACAACTTCCACAACTCCGTCCCCGAGGCGCTCGAACGCGTCCG
           **  *  ** **** ** **  * ***** **   *** **  * **  * **  *
  301" TAAGGTTTCGATCATCGATAATTTTGATAACTCTGTTATCGAAGCTGTTGATAGAGTTAG

  186' CCTCATCGCCGGGCCCGCGCTCTCCGCCCGCCTCGACTTCATCCGGGGGGATCTGAGGAG
           * *  ** ** *  ******      **********  * *** ***** ** *
  361" GGAGCTTGTTGGTCCTGATCTCTCCAAGAAGCTCGACTTCAATCTGGGTGATCTAAGAAA

  246' CGCCGGGGACTTGGAGAAGGCGTTCGCGGCCAGGAGGTACGACGCCGTCGTCCACTTCGC
       *   ****** * *****    *** *      *** *  ** ** **  * ** ** **
  421" CAAAGGGGACATTGAGAAACTATTCTCCAAGCAGAGATTTGATGCTGTGATTCATTTTGC
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306' GGGGCTCAAGGCCGTCGGGGAGAGCGTCGCGCGCCCGGACATGTACTACGAGAACAACCT
481" GGGTCTTAAAGCTGTGGGTGAGAGTGTTGAAAACCCTCGCCGCTACTTTGACAATAACTT

366' CGCCGGCACCATCAACCTCTACAAGGCCATGAACGAGCACGGCTGCAAGAAGATGGTGTT
541" GGTTGGAACAATCAATCTATATGAGACCATGGCAAAGTACAACTGCAAAATGATGGTGTT

426' CTCGTCGTCCGCGACCGTGTACGGCTGGCCGGAGGTGATCCCGTGCGTCGAGGACTCCAA
601" TTCATCTTCTGCCACTGTTTATGGACAACCTGAAAAGATTCCATGCATGGAAGACTTTGA

486' GCTGCAGGCCGCCAACCCCTACGGCAGGACCAAGCTCATCCTGGAGGAGTTGGCGCGGGA
661" ATTAAAGGCTATGAATCCTTATGGTCGTACTAAGCTCTTTCTTGAAGAAATAGCTAGAGA

546' CTACCAGCGCGCGGACCCGGGCTGGAGCATCGTCCTGCTGCGCTACTTCAACCCCATCGG
721" TATTCAAAAGGCAGAACCGGAATGGAGAATTATTCTGCTGAGGTACTTCAATCCTGTAGG

606' CGCCCACAGCTCCGGCGAGATCGGCGAGGACCCCAAGGGGGTGCCCAACAACCTGCTGCC
781" AGCACATGAGAGTGGCAGTATTGGTGAGGATCCAAAAGGCATCCCCAATAACCTCATGCC

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841" TTACATCCAACAAGTGGCCGTTGGACGTTTACCGGAACTCAATGTCTATGGACATGACTA

726' CCCCACCCGTGACGGCACCGCGATCAGGGACTACATACACGTCGTCGACCTGGCCGACGG
901" TCCCACCGAGGATGGTAGTGCGGTAAGAGACTACATCCATGTGATGGATTTAGCAGATGG

786' GCACATCGCGGCGCTGAACAAGCTGTTCGACACTCCTGATTTCGGTTGTGTGGCCTACAA
961" CCATATCGCTGCGCTCAGGAAGCTATTTGCTGATCCAAAGATTGGTTGTACTGCTTACAA

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1021" TCTAGGGACTGGTCAAGGAACGTCTGTGTTAGAAATGGTTGCAGCTTTTGAAAAAGCTTC

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1026' GATGTGCAGGGACCAGTGGAACTGGGCCAAGAAGAACCCCTATGGCTACTGCGGCACTGC
1201" GATGTGCAGAGATCAGTGGAAATGGGCAAACAATAATCCATGGGGTTACCAGAATAAGCT

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1261" TTGAATTTACTTCTTTTGTTTGGAGTTACCATTTCTAATTACTCAAATCTAAAAGAAAGA

[GENETYX-MAC: Multiple Alignment]
Date : 2007.07.26

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Doremann and Bennig DNA      1 ------------------------------------------------------------GA      2
Town et al UGE DNA           1 CCACTCATTTTTCCTATTTTTCGCTTTGCGTGCCTTCTTATCAACTTGTAAACAAAGCTA     60
PsUGE1                       1 ------------------------------------------------------------      1

Doremann and Bennig DNA      3 CAAATATCTTTAAATAAGGACCCAACTCTTTTTCAATTCCTCCCATCAATCTTCTTCATT     62
Town et al UGE DNA          61 CAAATATCTTTAAATAAGGACCCAACTCTTTTTCAATTCCTCCCATCAATCTTCTTCATT    120
PsUGE1                       1 ------------------------------------------------------------      1

Doremann and Bennig DNA     63 TGTTCTTCTGTTGGTGGTGGTGATCTAGTTTTCAAAGAATCGATTTTGCCAAGTGGGTTC    122
Town et al UGE DNA         121 TGTTCTTCTGTTGGTGGTGGTGATCTAGTTTTCAAAGAATCGATTTTGCCAAGTGGGTTC    180
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Doremann and Bennig DNA    123 TTCTTGATAACCTTTCTTCTTCTTTGAAATGGGTTCTT-CTGTGGAGCAGAACATTCTTG    181
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PsUGE1                       8 TCGGCGGGGCGGAGGG--GGGGGGGGGGGGGCGGGGGCGAGCGGCCG-GAGGGTGGCTGG     64

Doremann and Bennig DNA    182 TTACTGGTGGTGCTGGCTTTATCGGGACGCATACTGTTGTTCAACTTCTCAAAGATGGTT    241
Town et al UGE DNA         240 TTACTGGTGGTGCTGGCTTTATCGGGACGCATACTGTTGTTCAACTTCTCAAAGATGGTT    299
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Doremann and Bennig DNA    242 TTAAGGTTTCGATCATCGATAATTTTGATAACTCTGTTATCGAAGCTGTTGATAGAGTTA    301
Town et al UGE DNA         300 TTAAGGTTTCGATCATCGATAATTTTGATAACTCTGTTATCGAAGCTGTTGATAGAGTTA    359
PsUGE1                     125 ACGGCGTCAGCGTGGTCGACAACTTCCACAACTCCGTCCCCGAGGGCGCTCGAACGCGTCC    184

Doremann and Bennig DNA    302 GGGAGCTTGTTGGTCCTGATCTCTCCAAGAAGCTCGACTTCAATCTGGGTGATCTAAGAA    361
Town et al UGE DNA         360 GGGAGCTTGTTGGTCCTGATCTCTCCAAGAAGCTCGACTTCAATCTGGGTGATCTAAGAA    419
PsUGE1                     185 GCCTCATCGCCGGGGCGCGCGCTCTCGGCCCGCCTCGACTTCATCGGGGGGGATCTGAGGA    244

Doremann and Bennig DNA    362 ACAAAGGGGACATTGAGAAACTATTCTCCAAGCAGAGATTTGATGCTGTGATTCATTTTG    421
Town et al UGE DNA         420 ACAAAGGGGACATTGAGAAACTATTCTCCAAGCAGAGATTTGATGCTGTGATTCATTTTG    479
PsUGE1                     245 GGGCCGGGGGACTTGGAGAAGGCGTTCGGGGCCAGGAGGTACGACGCGCGTCGTCCACTTCG    304

Doremann and Bennig DNA    422 CGGGTCTTAAAGCTGTGGGTGAGAGTGTTGAAAAGGGTCGCCGCTACTTTGACAATAACT    481
Town et al UGE DNA         480 CGGGTCTTAAAGCTGTGGGTGAGAGTGTTGAAAACCCTCGCCGCTACTTTGACAATAACT    539
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Doremann and Bennig DNA    482 TGGTTGGAACAATCAATCTATATGAGACCATGGCAAAGTACAACTGCAAAATGATGGTGT    541
Town et al UGE DNA         540 TGGTTGGAACAATCAATCTATATGAGACCATGGCAAAGTACAACTGCAAAATGATGGTGT    599
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Doremann and Bennig DNA    542 TTTCATCTTCTGCCACTGTTTATGGACAACCTGAAAAGATTCCATGCATGGAAGACTTTG    601
Town et al UGE DNA         600 TTTCATCTTCTGCCACTGTTTATGGACAACCTGAAAAGATTCCATGCATGGAAGACTTTG    659
PsUGE1                     425 TCTCGTCGTCGGAGCGTGTACGGCTGGCCGGAGGTGATCCCGTGCGTCGAGGACTCCA    484

Doremann and Bennig DNA    602 AATTAAAGGCTATGAATCCTTATGGTCGTACTAAGCTCTTTCTTGAAGAAATAGCTAGAG    661
Town et al UGE DNA         660 AATTAAAGGCTATGAATCCTTATGGTCGTACTAAGCTCTTTCTTGAAGAAATAGCTAGAG    719
PsUGE1                     485 AGCTTGCAGGGCGCCAACCGCTACGGCAGGAGCAAGCTCATCCTGGAGGAGTTGGGGCGGG    544

Doremann and Bennig DNA    662 ATATTCAAAAGGCAGAACCGGAATGGAGAATTATTCTGCTGAGGTACTTCAATCCTGTAG    721
Town et al UGE DNA         720 ATATTCAAAAGGCAGAACCGGAATGGAGAATTATTCTGCTGAGGTACTTCAATCCTGTAG    779
PsUGE1                     545 ACTACCAGCGCGGGGACCCGGGCTGGAGCATCGTCCTGCTGCGCTACTTCAACCCCATCG    604

Doremann and Bennig DNA    722 GAGCACATGAGAGTGGCAGTATTGGTGAGGATCCAAAAGGCATCCCCAATAACCTCATGC    781
Town et al UGE DNA         780 GAGCACATGAGAGTGGCAGTATTGGTGAGGATCCAAAAGGCATCCCCAATAACCTCATGC    839
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Doremann and Bennig DNA    782 CTTACATCCAACAAGTGGCCGTTGGACGTTTACCGGAACTCAATGTCTATGGACATGACT    841
Town et al UGE DNA         840 CTTACATCCAACAAGTGGCCGTTGGACGTTTACCGGAACTCAATGTCTATGGACATGACT    899
PsUGE1                     665 GCTACATCCAGCAGGTCGCCGTCGGCAGGCTCCCCGAGCTCAACGTCTACGGCCACGATT    724

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Town et al UGE DNA         900 ATCCCACCGAGGATGGTAGTGCGGTAAGAGACTACATCCATGTGATGGATTTAGCAGATG    959
PsUGE1                     725 ACCCCACCCGTGACGGCACCGCGATCAGGGACTACATACACGTCGTCGACCTGGGCGACG    784

Doremann and Bennig DNA    902 GCCATATCGCTGCGCTCAGGAAGCTATTTGCTGATCCAAAGATTGGTTGTACTGCTTACA    961
Town et al UGE DNA         960 GCCATATCGCTGCGCTCAGGAAGCTATTTGCTGATCCAAAGATTGGTTGTACTGCTTACA   1019
PsUGE1                     785 GGCACATCGGGGCGCTGAACAAGCTGTTCGACACTCCGTGATTTCGGTTGTGTGGCCTACA    844

Doremann and Bennig DNA    962 ATCTAGGGACTGGTCAAGGAACGTCTGTGTTAGAAATGGTTGCAGCTTTTGAAAAAGCTT   1021
Town et al UGE DNA        1020 ATCTAGGGACTGGTCAAGGAACGTCTGTGTTAGAAATGGTTGCAGCTTTTGAAAAAGCTT   1079
PsUGE1                     845 ATCTGGGCACAGGGGGCGCGCACATCCGTTCTCGAGATGGTGGGGGGGTTCAAGAAGGGAT    904

Doremann and Bennig DNA   1022 CCGGCAAGAAAATCCCGATTAAGCTCTGTCCGAGAAGGTCAGGAGATGCAACAGCAGTTT   1081
Town et al UGE DNA        1080 CCGGCAAGAAAATCCCGATTAAGCTCTGTCCGAGAAGGTCAGGAGATGCAACAGCAGTTT   1139
PsUGE1                     905 CCGGCAAGGAGATCCCCACCAAGATGTGCCCCAGGAGACCGGGGTGACGCGACGGAGGTTT    964

Doremann and Bennig DNA   1082 ATGCTTCAACAGAGAAGGCTGAGAAAGAACTTGGCTGGAAGGCAAAATATGGAGTGGATG   1141
Town et al UGE DNA        1140 ATGCTTCAACAGAGAAGGCTGAGAAAGAACTTGGCTGGAAGGCAAAATATGGAGTGGATG   1199
PsUGE1                     965 ACGGGTCCACTGAGAAGGGCGAAAGGGAGCTCGGATGGAGGGGCCAGTATGGAATCGAGG   1024

Doremann and Bennig DNA   1142 AGATGTGCAGAGATCAGTGGAAATGGGGTTTCAATAATCCATGGGGTTACCAGAATAAGC   1201
Town et al UGE DNA        1200 AGATGTGCAGAGATCAGTGGAAATGGGCAAACAATAATCCATGGGGTTACCAGAATAAGC   1259
PsUGE1                    1025 AGATGTGCAGGGACCAGTGGAACTGGGCCAAGAAGAACCCCTATGGCTACTGCGGCACTG   1084

Doremann and Bennig DNA   1202 TTTGAATTTACTTCTTTTGTTTGGAGTTACCATTTCTAATTACTCAAATCTAAAAGAAAG   1261
Town et al UGE DNA        1260 TTTGAATTTACTTCTTTTGTTTGGAGTTACCATTTCTAATTACTCAAATCTAAAAGAAAG   1319
PsUGE1                    1085 CCGAAAAATA----------------------------------------------------   1094

Doremann and Bennig DNA   1262 AAATATACATACATATGATGATATAGTTGTGCTTTATATTCCACATGTATCGAACTGATC   1321
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PsUGE1                    1094 ------------------------------------------------------------   1094

Doremann and Bennig DNA   1322 TCTTACTTCGATGAATAAAATGGAAAGTTGATTTA------------------------   1356
Town et al UGE DNA        1380 TCTTACTTCGATGAATAAAATGGAAAGTTGATTTGATTGAATTTTTAGTTTTCTTTCACT   1439
PsUGE1                    1094 ------------------------------------------------------------   1094

Doremann and Bennig DNA   1356 ----------------------                                       1356
Town et al UGE DNA        1440 GAATAAAAAGGCTTGTTCAATGG                                      1462
PsUGE1                    1094 ----------------------                                       1094
```

```
[ GENETYX-MAC : Amino Acid Sequence Homology Data ]

Date : 2007.07.27

1st Amino Acid Sequence
  File Name         : PsUGE1TRANSLATE
  Sequence Size     : 364

2nd Amino Acid Sequence
  File Name         : Doremann bennig translate
  Sequence Size     : 351

  Unit Size to compare = 2
  Pick up Location     = 5


[71.1% / 346 aa]
     INT/OPT.Score : <   1348/  1356 >

     1' MAIGGAEAGGGGAGASGRSVLVTGGAGFIGTHTALRLLEQGYGVTVVDNFHNSVPEALER
                  ... ....************...**..*. *...***.*** **..*
      1"             MGSSVEQNILVTGGAGFIGTHTVVQLLKDGFKVSIIDNFDNSVIEAVDR

     61' VRLIAGPALSARLDFIRGDLRSAGDLEKAFAARRYDAVVHFAGLKAVGESVARPDMYYEN
         **  ..**.**  .***  ****. **.** *. .*.***.***********..  .*..*
     50" VRELVGPDLSKKLDFNLGDLRNKGDIEKLFSKQRFDAVIHFAGLKAVGESVEKGRRYFDN

    121' NLAGTINLYKAMNEHGCKKMVFSSSATVYGWPEVIPCVEDSKLQAANPYGRTKLILEELA
         **.******..*....**.********** ** ***.** .*.* *******.***.*
    110" NLVGTINLYETMAKYNCKMMVFSSSATVYGQPEKIPCMEDFELKAMNPYGRTKLFLEEIA

    181' RDYQRADPGWSIVLLRYFNPIGAHSSGEIGEDPKGVPNNLLPYIQQVAVGRLPELNVYGH
         ** *.*.*.*.*.*******.***.**.******.****.******************
    170" RDIQKAEPEWRIILLRYFNPVGAHESGSIGEDPKGIPNNLMPYIQQVAVGRLPELNVYGH

    241' DYPTRDGTAIRDYIHVVDLADGHIAALNKLFDTPDFGCVAYNLGTGRGTSVLEMVAAFKK
         **** **.*.******.*********.***..*..**.******.**********.*
    230" DYPTEDGSAVRDYIHVMDLADGHIAALRKLFADPKIGCTAYNLGTGQGTSVLEMVAAFEK

    301' ASGKEIPTKMCPRRPGDATEVYASTEKAERELGWRAQYGIEEMCRDQWNWAKKNPYGYCG
         ****.**.*.****.****.********.****.*.**..*******.**  .**.**
    290" ASGKKIPIKLCPRRSGDATAVYASTEKAEKELGWKAKYGVDEMCRDQWKWAFNNPWGYQN

    361' TAEK

    350" KL
```

```
1st Amino Acid Sequence
  File Name         : PsUGE1TRANSLATE
  Sequence Size     : 364

2nd Amino Acid Sequence
  File Name         : Town et al. UGE
  Sequence Size     : 351

  Unit Size to compare = 2
  Pick up Location     = 5


[71.4% / 346 aa]
     INT/OPT.Score : <   1358/  1366 >

     1' MAIGGAEAGGGGAGASGRSVLVTGGAGFIGTHTALRLLEQGYGVTVVDNFHNSVPEALER
                  ... ....************...**..*. *...***.*** **..*
      1"             MGSSVEQNILVTGGAGFIGTHTVVQLLKDGFKVSIIDNFDNSVIEAVDR
```

```
 61' VRLIAGPALSARLDFIRGDLRSAGDLEKAFAARRYDAVVHFAGLKAVGESVARPDMYYEN
     ** ..**.** .***  ****. **.** *. .*.***.***********..* .*..*
 50" VRELVGPDLSKKLDFNLGDLRNKGDIEKLFSKQRFDAVIHFAGLKAVGESVENPRRYFDN

121' NLAGTINLYKAMNEHGCKKMVFSSSATVYGWPEVIPCVEDSKLQAANPYGRTKLILEELA
     **.******..*....**.********** ** ***.** .*.* ********.***.*
110" NLVGTINLYETMAKYNCKMMVFSSSATVYGQPEKIPCMEDFELKAMNPYGRTKLFLEEIA

181' RDYQRADPGWSIVLLRYFNPIGAHSSGEIGEDPKGVPNNLLPYIQQVAVGRLPELNVYGH
     ** *.*.*.*.*.*******.***.**.*******.****.******************
170" RDIQKAEPEWRIILLRYFNPVGAHESGSIGEDPKGIPNNLMPYIQQVAVGRLPELNVYGH

241' DYPTRDGTAIRDYIHVVDLADGHIAALNKLFDTPDFGCVAYNLGTGRGTSVLEMVAAFKK
     **** **.*.******.**********.***..*..**.*******.**********.*
230" DYPTEDGSAVRDYIHVMDLADGHIAALRKLFADPKIGCTAYNLGTGQGTSVLEMVAAFEK

301' ASGKEIPTKMCPRRPGDATEVYASTEKAERELGWRAQYGIEEMCRDQWNWAKKNPYGYCG
     ****.**.*.****.****.********.****.*.**..*******.**..**.**
290" ASGKKIPIKLCPRRSGDATAVYASTEKAEKELGWKAKYGVDEMCRDQWKWANNNPWGYQN

361' TAEK

350" KL
```

```
1st Amino Acid Sequence
  File Name         : PsUGE1TRANSLATE
  Sequence Size     : 364

2nd Amino Acid Sequence
  File Name         : Rosa Patent amino acid
  Sequence Size     : 363

  Unit Size to compare = 2
  Pick up Location     = 5
```

```
[90.1% / 365 aa]
     INT/OPT.Score : <   1028/  1662 >

   1' MAIGGAEAGGGGAGASGRSVLVTGGAGFIGTHTALRLLEQGYGVTVVDNFHNSVPEALER
      *****.******** * ****************.*******  ***************.*
   1" MAIGGSEAGGGGAG-SMRSVLVTGGAGFIGTHTVLRLLEQGTIVTVVDNFHNSVPEALDR

  61' VRLIAGPALSARLDFIRGDLRSAGDLEKAFAARRYDAVVH-FAGLKAVGESVARPDMYYE
      **********.**********...****.*********.* ***********.*.****
  60" VRLIAGPALSTRLDFIRGDLRNTDDLEKVFAARRYDAVIHPFAGLKAVGESVAHPEMYYE

 120' NNLAGTINLYKAMNEHGCKKMVFSSSATVYGWPEVIPCVEDSKLQAANPYGRTKLILEEL
      *** ******.*.******.**********************************..
 120" NNLIGTINLYKSMKEHGCKKLVFSSSATVYGWPEVIPCVEDSKLQAANPYGRTKLILEDM

 180' ARDYQRADPGWSIVLLRYFNPIGAHSSGEIGEDPKGVPNNLLPYIQQVAVGRLPELNVYG
      ****.***..**********************.*************** *.*****
 180" ARDYHRADTEWSIVLLRYFNPIGAHSSGEIGEDPKGIPNNLLPYIQQVAVGRAPXLNVYG

 240' HDYPTRDGTAIRDYIHVVDLADGHIAALNKLFDTPDFGCVAYNLGTGRGTSVLEMVAAFK
      **************************.****.**.**********************
 240" HDYPTRDGTAIRDYIHVVDLADGHIAALKKLFDSPDIGCVAYNLGTGRGTSVLEMVAAFK

 300' KASGKEIPTKMCPRRPGDATEVYASTEKAERELGWRAQYGIEEMCRDQWNWAKKNPYGYC
      **********.***** ****************.**************************
 300" KASGKEIPTKLCPRRP-DATEVYASTEKAERELAWRAQYGIEEMCRDQWNWAKKNPYGYC

 360' GTAEK
      *.*.*
 359" GGAKK
```

[GENETYX-MAC: Multiple Alignment]
Date : 2007.07.27

```
PsUGE1amino acids                   1 MAIGGAEAGGGGAGASGRSVLVTGGAGFIGTHTALRLLEQGGYGMTVVDNFHNSVPEALER   60
Town et al. UGE amino acids         1 -------MGS---SVEQN-ILVTGGAGFIGTHTVVQLLKDGFKMSIIDNFDNSVIEAVDR   49
Doremann& Bennig amino acids        1 -------MGS---SVEQN-ILVTGGAGFIGTHTVVQLLKDGFKMSIIDNFDNSVIEAVDR   49
Rosa Patent amino acids             1 MAIGGSEAGGGGAGSMR-SVLVTGGAGFIGTHTVLRLLEQGTIMTVVDNFHNSVPEALDR   59

PsUGE1amino acids                  61 VRL-IAGPALSARLDFIRGDLRSAGDLEKAFAARRYDAVVH-FAGLKAVGESVARPDMMY   118
Town et al. UGE amino acids        50 VRELV-GPDLSKKLDFNLGDLRNKGDIEKLFSKQRFDAVIH-FAGLKAVGESVENPRRYF   107
Doremann& Bennig amino acids       50 VRELV-GPDLSKKLDFNLGDLRNKGDIEKLFSKQRFDAVIH-FAGLKAVGESVEKGRRYF   107
Rosa Patent amino acids            60 VRL-IAGPALSTRLDFIRGDLRNTDDLEKVFAARRYDAVIHPFAGLKAVGESVAHPEMYY   118

PsUGE1amino acids                 119 ENNLAGTINLYKAMNEHGCKKMVFSSSATVYGWPEVIPCVEDSKLQAANPYGRTKLILEE   178
Town et al. UGE amino acids       108 DNNLVGTINLYETMAKYNCKMMVFSSSATVYGQPEKIPCMEDFELKAMNPYGRTKLFLEE   167
Doremann& Bennig amino acids      108 DNNLVGTINLYETMAKYNCKMMVFSSSATVYGQPEKIPCMEDFELKAMNPYGRTKLFLEE   167
Rosa Patent amino acids           119 ENNLIGTINLYKSMKEHGCKKLVFSSSATVYGWPEVIPCVEDSKLQAANPYGRTKLILED   178

PsUGE1amino acids                 179 LARDYQRADPGWSIVLLRYFNPIGAHSSGEIGEDPKGVPNNLLPYIQQVAVGRLPELNVY   238
Town et al. UGE amino acids       168 IARDIQKAEPEWRIILLRYFNPVGAHESGSIGEDPKGIPNNLMPYIQQVAVGRLPELNVY   227
Doremann& Bennig amino acids      168 IARDIQKAEPEWRIILLRYFNPVGAHESGSIGEDPKGIPNNLMPYIQQVAVGRLPELNVY   227
Rosa Patent amino acids           179 MARDYHRADTEWSIVLLRYFNPIGAHSSGEIGEDPKGIPNNLLPYIQQVAVGRAPKLNVY   238

PsUGE1amino acids                 239 GHDYPTRDGTAIRDYIHVVDLADGHIAALNKLFDTPDFGCVAYNLGTGRGTSVLEMVAAF   298
Town et al. UGE amino acids       228 GHDYPTEDGSAVRDYIHVMDLADGHIAALRKLFADPKIGCTAYNLGTGQGTSVLEMVAAF   287
Doremann& Bennig amino acids      228 GHDYPTEDGSAVRDYIHVMDLADGHIAALRKLFADPKIGCTAYNLGTGQGTSVLEMVAAF   287
Rosa Patent amino acids           239 GHDYPTRDGTAIRDYIHVVDLADGHIAALKKLFDSPDIGCVAYNLGTGRGTSVLEMVAAF   298

PsUGE1amino acids                 299 KKASGKEIPTKMCPRRPGDATEVYASTEKAERELGWRAQYGIEEMCRDQWNWAKKNPYG-   357
Town et al. UGE amino acids       288 EKASGKKIPIKLCPRRSGDATAVYASTEKAEKELGWKAKYGVDEMCRDQWKWANNNPWGY   347
Doremann& Bennig amino acids      288 EKASGKKIPIKLCPRRSGDATAVYASTEKAEKELGWKAKYGVDEMCRDQWKWAFNNPWGY   347
Rosa Patent amino acids           299 KKASGKEIPTKLCPRRPDAT-EVYASTEKAERELAWRAQYGIEEMCRDQWNWAKKNPYG-   356

PsUGE1amino acids                 358 --YCGTAEK                                                        364
Town et al. UGE amino acids       348 QNKL-----                                                        351
Doremann& Bennig amino acids      348 QNKL-----                                                        351
Rosa Patent amino acids           357 --YCGGAKK                                                        363
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